FIGURE 1

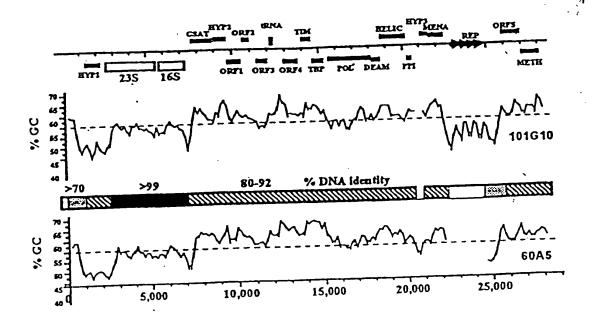


FIGURE 2

Seq. ID										
No.	Gene	Strain		TATA BOX			Coding Start		TATA to Start (bp	
81 82	Hypoth 03	A B	AAGCTAGACT AAGCTAAACT	TAATTT TAATTT	TGGG TGGG	ATCCGGCGGG ATCCGGCGAG	GCGGCGCATG CCGGCGCGTG			25
83 84	Hypoth 02	A B	GGAAACTTTG GGAAACTTTG	ATTATA ATTATA	CGGG CGGG	CGTGCTGCCC CGTACATTCC	CGGGGCCCAT	G		26
85	ORF 02	A B	AAGGCAAGGT ACGGCAAGGT	AATAAT AATAAT	AGCC AGCC	TGCCGTCTGT TGCCGTCCGT	AACGGCCGTA ACCTGCCGTA	TG		27
86 87 88	ORP 03	A B	CATGGAACTA	GATATT	AACC	GGTTCCGCGG	ATCCCATGCA	TG	~~~~	27
89 90	PPI	A B	ATACCGAGAA	GTTATA	GCAG	GGTATGGAAT	GTGCGCGCGC	ATG	~~~~~~~	28
91	GSAT	A	ATCCGCCCTG	ATTAAA	TTAT	GGGGGGAGCG	GCCTGCTGCC	GTG		28
92 93	ORF 05	B A	CCTTCATACA	CATAAA	TCCC	GCTTGGATGT	GCGGCTGCGC	ATG		28
94 95	deaminase	B	. GGCATATAC	CATAAT	ATGC	CGGGCGGTGG	CACCATGGCC	GTTG		29
96 97	RNA helic	B A	TGTACGAAAC	CATAAA	ACAA	CAGGCCGCGT	CAGGGCCGCG	.GTG		29
98 99	ORF 06	B A	ACACGCAG	AAATAT	CGGG	GGCCCGGGCG	GCGCGTATCA	CGTG		29
100 101	tRNA-tyr	B A	GCGATAGTTA	TTTAAA	ACTA	GGATGCCGAT	CACGGATCGT	CCCA		29
102 103	ТВР	B A	CCGGGCCCCG	GTTAAA	ATAG	CG.CACGGGC	GGATCCTGAC	CCCA		30
104 105	TIM	B A	GCGTCGATAG	AATAA	TACG	CGCAGGGGGC	CCCGTGGCGC	CAATG GATCGCCCGT	G	36
106 107	нуроth 01	B A	ATTTCAACTA	CATAAA	TGCC	TAGTTACGCA	GAAATAGCAA	GATCGCCCGT ACGACGTACT	TCGACTAATG	45
108 109	ORF 01	B A	ACGGCAGGCT	ATTATT	ACCT	TGCCTTGCGT	TGTA //G	ACAAAGTACT CGGGGTGCGG	CAGGGGATG	52
110 111	Methylase	B A	CTACAACGAT	TTTAAG	TCGG	CGCCGGGGCA	GCCG.//G	AGGGGGCCTG ATGTGGGGCA	GGCAACATG	104
112 113	165 RNA	В	CTACAAAGAT	TTTAAG	ACGG	CGCGGGTGCC	GCGG.//T	GGCACGGGGG CGTACGTGAC	CCTATCTTG	220
114	Archaeal	В	CCGGCGATGG	TITATA	TGCC	CATGGACAAG	GCGATCCGAT	CGTACGTGAC	GC.//AAT	
	consensus			YTTAWA						

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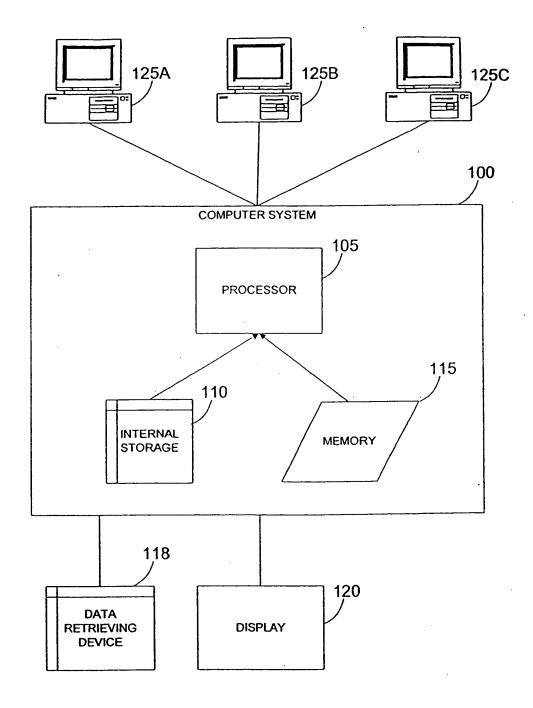
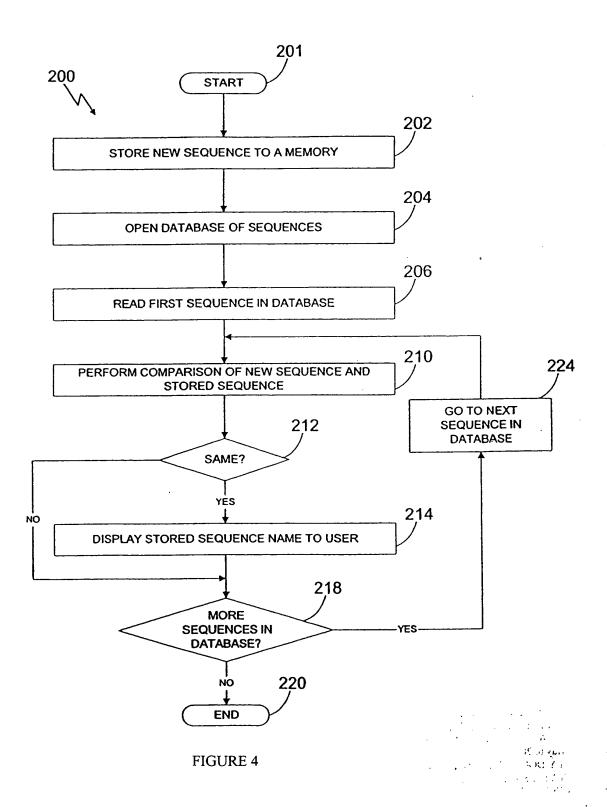
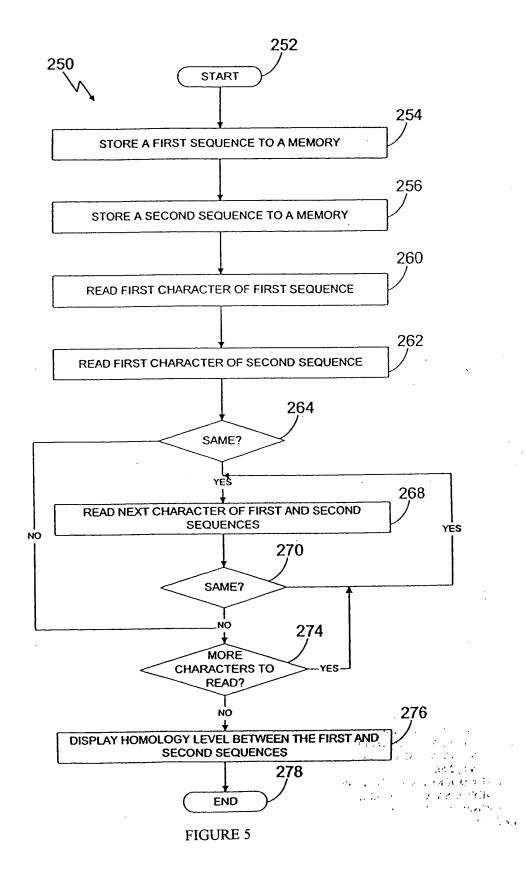


FIGURE 3





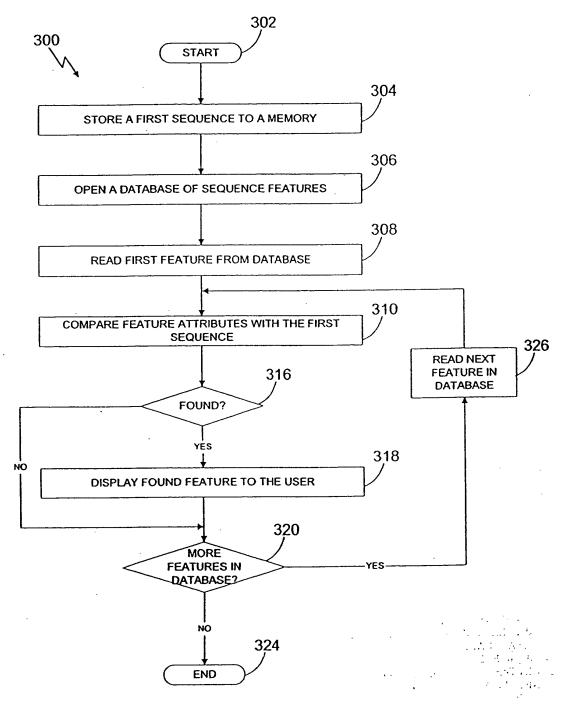


FIGURE 6